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Range: from  to   Reverse complemented strand Features:

1: AY039589. Reports *Arabidopsis thali...* [gi:14517507]

Links

Comment Features Sequence

LOCUS AY039589 685 bp mRNA linear PLN 20-JUN-2001  
 DEFINITION *Arabidopsis thaliana* AT4g02380/T14P8\_2 mRNA, complete cds.  
 ACCESSION AY039589  
 VERSION AY039589.1 GI:14517507  
 KEYWORDS FLI\_CDNA.  
 SOURCE *Arabidopsis thaliana* (thale cress)  
 ORGANISM *Arabidopsis thaliana*  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.  
 REFERENCE 1 (bases 1 to 685)  
 AUTHORS Kim,C.J., Chen,H., Cheuk,R., Koesema,E., Meyers,M.C., Banh,J.,  
 Bowser,L., Carninci,P., Dale,J.M., Gibson,H.A., Goldsmith,A.D.,  
 Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A.,  
 Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,  
 Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J.,  
 Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A.,  
 Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Yu,S., Shinozaki,K.,  
 Davis,R.W., Theologis,A. and Ecker,J.R.  
 TITLE *Arabidopsis* cDNA clones  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 685)  
 AUTHORS Kim,C.J., Chen,H., Cheuk,R., Koesema,E., Meyers,M.C., Banh,J.,  
 Bowser,L., Carninci,P., Dale,J.M., Gibson,H.A., Goldsmith,A.D.,  
 Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A.,  
 Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,  
 Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J.,  
 Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A.,  
 Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Yu,S., Shinozaki,K.,  
 Davis,R.W., Theologis,A. and Ecker,J.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-JUN-2001) Salk Institute Genomic Analysis Laboratory  
 (SIGnAL), Plant Biology Laboratory, The Salk Institute for  
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
 USA  
 COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
 Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.  
 The Salk, Stanford, PGEC (SSP) Consortium members carried out the  
 sequencing and annotation of the RAFL cDNAs: Shinn,P., Chen,H.,

Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J. Bowser,L., Dale,J.M., Gibson,H.A., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.

Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES	Location/Qualifiers
source	1..685 <i>/organism="Arabidopsis thaliana"</i> <i>/mol_type="mRNA"</i> <i>/db_xref="taxon:3702"</i> <i>/chromosome="4"</i> <i>/clone="RAFL03-07-M07(R12809)"</i> <i>/ecotype="Columbia"</i>
<u>5'UTR</u>	1..189
<u>CDS</u>	190..483 <i>/note="unknown protein"</i> <i>/codon_start=1</i> <i>/product="AT4g02380/T14P8_2"</i> <i>/protein_id="AAK62644.1"</i> <i>/db_xref="GI:14517508"</i> <i>/translation="MARSISNVKIVSAFVSRELSNAIFRRGYAATAAQGSVSSGRSGAVASAVMKKGVVEESTQKISWVPDPKTGYYRPETGSNEIDAAELRAALLNNKQ"</i>
<u>3'UTR</u>	484..685
ORIGIN	<pre> 1 tcatctcttc aaaccatttt cgaaagcctt gagagagaga acacagacga taccactt  61 cttcaatctc gttgcgcag tataatttac tcattcctcg gatatatctc tccttctgcg 121 gccccacaa gaagctacaa gaataaaaag tctgtttct ctctttcaa gaaaccactt 181 acttcgaaaa tggctcgttc tatctctaac gttaagatcg tatctgctt cgtctctcg 241 gaactctcca atgctatctt ccgacgtgt tatgcggcca cggcggcgca agggagcggt 301 tcgagcgttg gaagaagtgg agctgttgc tcggctgtga tgaagaagaa gggagtggaa 361 gaatcaaccc agaagatttc ttgggttcca gatccaaaa ccggttattt cagacccgaa 421 accggttcca acgagattga cgcggctgag ctacgagcag ctctttgaa caacaagcag 481 tgattgatta ttattacatg taattttgtc aaggcttta agaggagatt agtgggtaat 541 gatctggtgc agtgaaccct atttcataat gttaagtgcg gttctgtat gaataaaata 601 gagaagcgtt tggttcctc taattgtaac aaaaggatcg ttggatgtat gatagagttt 661 ttcttataaaa accatttcag aactt </pre>

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